Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

Claims 1 through 10 are cancelled.

11. (Original) A device for simultaneously detecting the presence of a plurality of different, non-nucleic acid target molecules in a sample, the device comprising:

a solid support; and

a plurality of different aptamer beacons bound to the support, each aptamer beacon having a first end attached to the support, and a binding region that binds to a specific non-nucleic acid target molecule, wherein the binding regions of different aptamer beacons bind to different target molecules.

12. (Original) The device of claim 11, wherein the solid support comprises a glass surface to which the first ends of the aptamer beacons are covalently bound.

13. (Original) The device of claim 11, wherein the solid support comprises a planar surface, and the aptamer beacons are distributed on the planar surface in a two-dimensional array.

14. (Original) The device of claim 13, wherein spots of identical aptamer beacons are located at different points in the two-dimensional array.

15. (Original) The device of claim 11, wherein the binding region of at least one of the aptamer beacons is configured to bind to a non-nucleic acid target molecule selected from the group consisting of a protein, a steroid, and an inorganic molecule.

16. (Original) The device of claim 11, wherein the aptamer beacons comprise RNA, DNA, modified RNA, modified RNA, or a combination thereof.

17. (Original) The device of claim 11, wherein each aptamer beacon comprises a reporter group for signaling binding of a target molecule to the binding region.

18. (Original) The device of claim 17, wherein the reporter group comprises a fluorophore.

19. (Presently Amended) A method of detecting the presence or absence of one or more different target molecules in a sample, the method comprising:

obtaining a plurality of aptamer beacons ~~of claim 1~~;

contacting the sample to the aptamer beacons, such that any target molecules in the sample can bind to corresponding binding regions of the aptamer beacons; and

detecting the presence of target molecules bound to the aptamer beacons,

wherein each of the aptamer beacons comprises:

an oligonucleotide comprising a loop portion, a first segment, and a second segment complementary to the first segment, wherein the first and second segments connected by the loop portion form a stem portion when hybridized together;

wherein a portion of the oligonucleotide comprises a binding region that has a secondary or tertiary conformation that changes to a different secondary or tertiary conformation upon specifically binding to the non-nucleic acid target molecule;

a first reporter moiety attached to the first segment; and

a second reporter moiety attached to the second segment, wherein the first and second reporter moieties interact to produce a detectable signal when the distance between them is changed;

wherein specific binding of the target molecule to the binding region causes a change in conformation of the aptamer beacon that separates the first and second segments, thereby altering the distance between the first and second reporter moieties, and produces a detectable signal.

20. (Original) The method of claim 19, wherein the aptamer beacons are in a liquid.

21. (Original) The method of claim 19, wherein the aptamer beacons are bound to a solid support.

22. (Original) The method of claim 19, wherein the solid support is a particle.

23. (Original) The method of claim 19, wherein the solid support is a plate.

24. (Original) The method of claim 19, wherein the aptamer beacons emit fluorescent radiation when excited by evanescent waves.

25. (Original) The method of claim 23, wherein different spots, each spot comprising a plurality of identical aptamer beacons, are distributed on the solid support in a predetermined array, and the method further comprises comparing a fluorescence pattern of the sample to known fluorescence patterns.

26. (Original) The method of claim 25, wherein the comparing step includes the use of a computer program, disposed on a computer readable medium, the computer program including instructions for causing a processor to:

compare the fluorescence pattern of the sample to a library of known fluorescence patterns; and

select the combination of known fluorescence patterns that most closely matches the fluorescence pattern of the sample.

27. (Original) The method of claim 19, wherein the detecting step includes detecting a change in the Raman emission frequencies of an aptamer beacon, the change caused by binding of a target molecule to the aptamer beacon.

28. (Original) The method of claim 23, wherein the solid support comprises a metal film to which the aptamers are bound, and the detecting step includes detecting a change in the resonant condition of surface plasmons in the metal film caused by binding of a target molecule to an aptamer beacon.

29. (Original) A computer program, disposed on a computer-readable medium, for analyzing the output of an assay that determines the composition of a sample and deduces the presence or absence of known abnormal conditions, the computer program including instructions for causing a processor to:

compare the assay output to a library of known outputs corresponding to subjecting samples of known composition to the assay;

select a combination of known outputs that most closely matches the assay outputs;

compare any deviation between the sample output and the combination of known outputs to a library of known deviations, the known deviations being caused by known abnormal conditions; and

deduce the presence or absence of known abnormal conditions.

30. (Original) The computer program of claim 29, wherein the known abnormal conditions include the presence of abnormal compounds in the sample, and the presence of normal compounds in abnormal quantities.

31. (Original) The computer program of claim 29, wherein the assay output and the known outputs comprise images.

32. (Original) A method for analyzing the output of an assay that determines the composition of a sample and deduces the presence or absence of known abnormal conditions, the method comprising:

comparing the assay output to a library of known outputs corresponding to subjecting samples of known composition to the assay;

selecting a combination of known outputs that most closely matches the assay outputs;

comparing any deviation between the sample output and the combination of known outputs to a library of known deviations, the known deviations being caused by known abnormal conditions; and

deducing the presence or absence of known abnormal conditions.

33. (Original) A device for detecting the presence of a target molecule in a sample, the device comprising:

a solid support; and

a plurality of different aptamer beacons bound to the support, each aptamer beacon having a first end attached to the support, and a binding region that binds to a specific enantiomer of the target molecule or a specific binding site of the target molecule, wherein the binding regions of different aptamer beacons bind to different enantiomers of the target molecule or to different binding sites of the target molecule.

34. (Original) The device of claim 33, wherein the target comprises an antigen, and the different binding sites comprise different epitopes of the antigen.

35. (Original) The device of claim 33, wherein the target comprises a bacteria, and the different binding sites comprise different surface proteins of the bacteria.

36. (Presently Amended) A system for simultaneously detecting the presence of a plurality of different non-nucleic acid target molecules in a sample, the system comprising:

a plurality of different aptamer beacons ~~of claim 1,~~; ~~each aptamer beacon having a first end attached to the support, a binding region that binds to a specific non-nucleic acid target molecule, the binding regions of different aptamers binding to different target molecules;~~ and

a detection system that detects the presence of target molecules bound to aptamer beacons, the detection system comprising a radiation source and a detector,

wherein each of the aptamer beacons comprises:

an oligonucleotide comprising a loop portion, a first segment, and a second segment complementary to the first segment, wherein the first and second segments connected by the loop portion form a stem portion when hybridized together;

wherein a portion of the oligonucleotide comprises a binding region that has a secondary or tertiary conformation that changes to a different secondary or tertiary conformation upon specifically binding to the non-nucleic acid target molecule;

a first reporter moiety attached to the first segment; and

a second reporter moiety attached to the second segment, wherein the first and second reporter moieties interact to produce a detectable signal when the distance between them is

changed;

wherein specific binding of the target molecule to the binding region causes a change in conformation of the aptamer beacon that separates the first and second segments, thereby altering the distance between the first and second reporter moieties, and produces a detectable signal; and

wherein each aptamer beacon has a first end attached to the support, a binding region that binds to a specific non-nucleic acid target molecule, the binding regions of different aptamers binding to different target molecules.

37. (Original) The system of claim 36, wherein the radiation source comprises a laser.

38. (Original) The system of claim 36, further comprising an analyzer to determine the presence of target molecules in the sample based on the output of the detector, wherein the analyzer comprises a computer processor programmed to:

compare the output of the detector to a library of known outputs corresponding to exposing samples of known composition to the aptamer beacons; and

select a combination of known outputs that most closely matches the assay outputs.

39. (Original) The system of claim 36, wherein the aptamer beacons are in a liquid.

40. (Original) The system of claim 36, wherein the aptamer beacons are attached to a solid support.

Claims 41 and 42 are cancelled.

43. (Presently Amended) A system for simultaneously detecting the presence of a plurality of different non-nucleic acid target molecules in a sample, the system comprising:

a plurality of different species of aptamer beacons ~~of claim 1,~~; ~~wherein each species of aptamer beacons has a different reporter group, a binding region that binds to a specific non-nucleic acid target molecule, and wherein the binding regions of different aptamers bind to different target molecules;~~ and

a detection system that detects the presence of target molecules bound to aptamer beacons, the detection system being able to detect the different reporter groups,

wherein each of the aptamer beacons comprises:

an oligonucleotide comprising a loop portion, a first segment, and a second segment complementary to the first segment, wherein the first and second segments connected by the loop portion form a stem portion when hybridized together;

wherein a portion of the oligonucleotide comprises a binding region that has a secondary or tertiary conformation that changes to a different secondary or tertiary conformation upon specifically binding to the non-nucleic acid target molecule;

a first reporter moiety attached to the first segment; and

a second reporter moiety attached to the second segment, wherein the first and second reporter moieties interact to produce a detectable signal when the distance between them is changed;

wherein specific binding of the target molecule to the binding region causes a change in conformation of the aptamer beacon that separates the first and second segments, thereby altering the distance between the first and second reporter moieties, and produces a detectable signal; and

wherein each species of aptamer beacons has a different reporter group, a binding region that binds to a specific non-nucleic acid target molecule, and wherein the binding regions of different aptamers bind to different target molecules.